SEARCH REQUEST FORM

a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed 99-62	Search Site	Venuors
Searcher: Belevines	TO STIC	IG Suite
Terminal time: 20	EM-L	STN
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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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MEDLINE
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                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2214)
Soh,J., Donnelly,R.J., Kotenko,S., Mariano,T.M., Cook,J.R., Wang,N., Emanuel,S.L., Schwartz,B., Miki,T. and Pestka,S. Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor 2011 76, 793-802 (1994)
Submitted (01-FEB-1994) Sidney Pestka, UMDNJ-Robert Wood Johnson
                                                                                                                                                                                                                                                                                                                                                  U05875.1 GI:463549
                     Pestka,S.
Direct Submission
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Result No.

Query Score Match Length DB ID

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AGFPMDFNVTLRLRAELGALHSAWVTMPWFQHYRNVTVGPPENIEVTPGEGSLIIRFS
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/db_xref="taxon:9606"
/clone="pSK1"
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/db_xref="GI:463550"
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/note="second chain of the receptor"
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                                                                                                      Local Similarity
1 GTTGACTGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCCCCACTGCACTCCAGCCTGGTG 60
                         1 gttgactggaggcggaggttgcagtgagccgagatcgccccactgcactccagcctggtg 60
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Accessory factory function for interferon gamma and its receptor Patent: US 6287853-A 3 11-SEP-2001;
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              1081 AACATTGAGGTGACCCCAGGAGAAGGCTCCCTCATCATCAGGTTCTCCCTCTCCCTTTGAC 1140
                                                                                          1021 GCCTGGGTGACAATGCCTTGGTTTCAACACTATCGGAATGTGACTGTCGGGCCTCCAGAA 1080
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2161 AATTTAAGATTTTGTTTTTAAACTGGAAATAAAAGATTGTATAGTGCATGTTTTT 2216
                                                                            2159 aatttaagattttgtttttaaactggaaataaaagattgtatagtgcatgttttt 2214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1740 tccagagaccagtattccc-tttttgctgcctctaaaaggcctgtccctgcagacatgaga 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1681 CCCACTGGCTCCCTGGAAGAGATCAAGCCATCGGAGCTGCTAGAGTTCTGTCTTGGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1621 TTTCCGGAAAAGGAGCAAGAAGATGTTCTCCAAACGCTTTGAACCAAAGCATGGGCCTAG 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1621 tttccggaaaaggagcaagaagatgttctccaaacgctttgaaccaaagcatgggcctag 1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1561 gccttggacaaggacagctcaccaaaggatgacgtctgggactctgtgtccattatctcg 1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1441 gcctgtttcttcctggtcctgaaatatagaggcctgattaaaatactggtttcacactcca 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1381 CTTCAGCAAGTCATCCTGATCTCCGTGGGAACATTTTCGTTGCTGGTGCTGGCAGGA 1440
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                                                                                                                                                                             2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1981 CATTATTGGTTGGGCTGAGCAGTCAGAAGACCTGGTCGTCGTCTTGACTTTGGCAAATGA 2040
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                                                                                                                                                                                                                                                                                                                                                                                                               cattattggttgggctgagcagtcagaagacctggtcgtcgtcttgactttggcaaatga 2038
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592 gcggaccccgagcggggccccgggccgcgacctgagccgcggcgcggggcccatg 651

532 ggcgggccctgcgccctgcgctcgccatggcggttttgggcggcgacgtgagcggctcc 591

GGCGGGCCCTGCGCCTCGCCATGGCGGTTTTGGGCGGCGACGTGAGCGGCTCC 68

Matches 1679; Query Match Best Local :

Conservative

 Mismatches Pred. No.

2; Indels

2; Gaps

2e-279;

Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC003624 1722 bp mRNA linear PRI 12-JUL-2 Homo sapiens, interferon gamma receptor 2 (interferon gamma transducer 1), clone MGC:2193 IMAGE:2967074, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL
Series: IRAL Plate: 3 Row: k Column: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1722)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             passed the following selection criteria: matched mRNA gi: 463551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.systemsbiology.org
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                                                                                                                                                                                                                                                                                                                  OTL
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/t-ans.lation="MREPTLIMSLL"
/t-ans.lation="MREPTLIMSL"
/t-ans.l
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SPFDIADTSTAFFCYYVHYWEKGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLW
NKSNIFRVGHLSNISCYETMADASTELQQVILISVGTFSLLSVLAGAGFFLYLKVRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MGC:2193 IMAGE:2967074"
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/clone_lib="NHH_MGC_20"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="LocusID:3460"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     IKYWFHTPPSIPLQIEEYLKDPTQPILEALDKDSSPKDDVWDSVSIISFPEKEQEDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="interferon gamma receptor 2 (interferon gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
75.2%;
99.8%;
                                                                                                                                                                                                                                                                     446 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Vector: pors7"
                                                                                                                                                                                                                                                               408 g
                                                        Score 1665.8;
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                                                                                                                                                                                                                                                                     423 t
                                                        DB 9;
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                                                   Length 1722;
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1149 TGGGCCTAGCCCACTGGCTCCCTGGAAGAGATCAAGCCATCGGAGCTGCTAGAGTTCTGT 1208
                                          1672 tgggcctagcccactggctccctggaagagatcaagccatcggagctgctagagttctgt 1731
                                                                                                                                                    1612 attatctcgtttccggaaaaggagcaagaagatgttctccaaaacgcttttgaaccaaagca 1671
                                                                                                                                                                                                                                     1029 ATCTTAGAGGCCTTGGACAAGGACAGCTCACCAAAGGATGACGTCTGGGGACTCTGTGTCC
                                                                                                                                                                                                                                                                    1552 atcttagaggccttggacaaggacagctcaccaaaggatgacgtctgggactctgtgtcc 1611
                                                                                                                                                                                                                                                                                                                                                                                                1492 cacactecaccaagcateccattacagatagaagagtatttaaaagacecaacteageee 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1132 ccctttgacatcgctgatacctccacggccttttttttgttattatgtccattactgggaa 1191
                                                                                                                         1089 ATTATCTCGTTTCCGGAAAAGGAGCAAGAAGATGTTCTCCAAACGCTTTGAACCAAAGCA 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1432 ctggcaggagcctgtttcttcctggtcctgaaatatagaggcctgattaaatactggttt 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1312 aacatotttagagtcgggcatttaagcaacatatcttgctacgaaacaatggcagatgcc 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1072 cctccagaaaacattgaggtgaccccaggagaaggctccctcatcatcatggttctcctct 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   789 AACATCTTTAGAGTCGGGCATTTAAGCAACATATCTTGCTACGAAACAATGGCAGATGCC
                                                                                                                                                                                                                                                                                                                                               969 CACACTCCACCAAGCATCCCATTACAGATAGAAGAGTATTTAAAAAGACCCAACTCAGCCC 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      849 TCCACTGAGCTTCAGCAAGTCATCCTGATCTCCGTGGGAACATTTTCGTTGCTGTCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             729 TTAAAACCCTCCAGAGTGTACTGTTTACAAGTCCAGGCACAACTGCTTTGGAACAAAGT 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             669 AAAGGAGGAATCCAACAGGTCAAAGGCCCTTTCAGAAGCAACTCCATTTCATTGGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          609 CCCTTTGACATCGCTGATACCTCCACGGCCTTTTTTTGTTATTATGTCCATTACTGGGAA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            952 tcagcaggcttcccaatggatttcaatgtcactctacgccttcgagctgagctgggagca 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   892 ataggggtgaattgtacacagatcacagcaacagagtgtgacttcactgccgccagtccc 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 CTCCATTCTGCCTGGGTGACAATGCCTTGGTTTCAACACTATCGGAATGTGACTGTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429 TCAGCAGGCTTCCCAATGGATTTCAATGTCACTCTACGCCTTCGAGCTGAGCTGGGAGCA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 ATAGGGGTGAATTGTACACAGATCACAGCAACAGAGTGTGACTTCACTGCCGCCAGTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCAGGAGCCTGTTTCTTCCTGGTCCTGAAATATAGAGGCCTGATTAAATACTGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1687 TTT 1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2152 tootagtaatttaagattttgtttttaaaottggaaataaaagattgtatagtgcatgttt 2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1972 cttttttcattattggttgggctgagcagtcagaagacctggtcgtcgtcttgactttgg 2031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soh, J., Donnelly, R.J., Kotenko, S., Mariano, T.M., Cook, J.R., Wang, N., Emanuel, S.L., Schwartz, B., Miki, T. and Pestka, S. Identification and sequence of an accessory factor required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                 Medical School, 675 Hoes
                                                                                                                                                                                                                                                                                                                                         Submitted (01-FEB-1994) Sidney
                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                Pestka,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation of the human interferon gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human clone pJS3 interferon gamma receptor accessory factor-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AF-1) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1566)
                                                                                                                                                                                                                                                                                                                                                                                                                           bases 1 to 1668)
/cell_type="B-cell precursor"
/note="clone pJS4 (pD5) was isolated from the same cDNA
library and is identical to pJS3 at base positions
27. .1629."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              793-802 (1994)
                                                                                                                                           /cell_line="Daudi"
                                                                                                                                                                      /clone="pJS3; pD9"
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                           Sidney Pestka, UMDNJ-Robert Wood Johnson
Lane, Piscataway, NJ 08854-5635, USA
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CDS
                                                        mat_peptide
1196 gaggaatccaacaggtcaaaggccctttcagaagcaactccatttcattggataacttaa 1255
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                                                                                                                                                                                                                                                                                                           1016 attctgcctgggtgacaatgccttggtttcaacactatcggaatgtgactgtcgggcctc 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656 cgacgctgctgtggtcgctgctgctgctcggagtcttcgccgccgccgccgccgccgcgccc 715
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                                                                                                                                                                                                                                                                                481 ATTCTGCCTGGGTGACAATGCCTTGGTTTCAACACTATCGGAATGTGACTGTCGGGCCTC 540
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Qvlswepvalsnstrpvvvqvqfkytdskwftadimsigvnctqitatecdftaasps
agfpmdfnvtlrlraelgalhsawvtwpwfqhyrnvtvgppenievtpgegsliirfs
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NKSNIFRVGHLSNISCYETMADASTELQQVILISVGTFSLLSVLAGACFFLVLKYRGL
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/note="second chain of the receptor"
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                     1360 atggcagatgcctccactgagcttcagcaagtcatcctgatctccgtgggaacattttcg 1419
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ATGGCAGATGCCTCCACTGAGCTTCAGCAAGTCATCCTGATCTCCGTGGGAACATTTTCG 783
                                                                                                 tggaacaaaagtaacatctttagagtcgggcatttaagcaacatatcttgctacgaaaca 1359
                                                                                                                                                                                                                                  CATTACTGGGAAAAAAGGAGGAATCCAACAGGTCAAAGGCCCTTTCAGAAGCAACTCCATT 603
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                                                                        TGGAACAAAAGTAACATCTTTAGAGTCGGGCATTTAAGCAACATATCTTGCTACGAAACA 723
                                                                                                                                                        TCATTGGATAACTTAAAAACCCTCCAGAGTGTACTGTTTACAAGTCCAGGCACAACTGCTT 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pestka,S., Kotenko,S., Soh,J., Donnelly,R.J., Mariano,T.M., Cook,J.R., Emanuel,S. and Schwartz,B. Accessory factory function for interferon gamma and its receptor Patent: US 6287853-A 2 11-SEP-2001;
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                  Rhee, S., Ebensperger, C., Dembic, Z. and Pestka, S.
The structure of the gene for the second chain of the human
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Human interferon-gamma receptor chain 2 (IFNGR2) gene, promoter
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interferon-gamma receptor
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/protein_id="AAC52066.1"
/db_xref="GI:1669506"
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/gene="IFNGR2"
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                                                                                                                                                                                                                                                                                                                                              Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
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Homo sapiens 30,438bp genomic DNA of 21q22.1
Published Only in DataBase (1999) In press
(bases 1 to 30438)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
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                                                                                                                                                                                                      The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical
                                                                                                                                                                                                                                                                                                                The sequence is a part of the data (ACCESSION No. AP000174 -
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/db_xref="taxon:9606"
/chromosome="21"
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     Hattori,M., Ishii,K., Toyoda,A., Shiba,T. Homo sapiens genomic DNA, Chromosome 21q Published Only in DataBase (1998) In press 2 (bases 1 to 100000)
                                                                                                                                                                                                                                                                                                             AP000045
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens genomic DNA, chromosome 21q22.1, segment 16/28
                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                        complete sequence.
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                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                           Homo sapiens DNA, clone:T1866-f90A8f_9.
                                                                                                                                                                                                                                                                                   AP000045.1 GI:3132355
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                                                                                     Toyoda, A., Shiba, T. and Sakaki, Y.
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                                                           25180 CGGCCGAGCCGAATCCCCTCCACCGGGACGCCCCGCTGCTGCTCGGGAAGAGGCGGGCCC 25239
                                                                                                                                                                                                                                                                                25060 GCGTGGGGTCCCCGCGCTGCAGCCGCAGAGGCCCCCCAGGGCCGCGTTCCCGGAGCGGG 25119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 32.3%; Score 716.2; DB 9; Length 100000; Local Similarity 99.6%; Pred. No. 1.4e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0028 Japan For further information about this sequence, including its locati and relationship to other sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp/;.
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Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax: +81-3-5449-5445.
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suh-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For further information about this sequence, including its locat and relationship to other sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/) or send email to webmaster@www.alis.tokyo.jst.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-APR-1999) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advance Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The sequence is submitted by Human Genome Sequencing in ALIS project of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens 2,051,516bp genomic DNA of 21q22.1 GART and AML region
Published Only in DataBase (1999) In press
2 (bases 1 to 100000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory as a JST sequencing team. Principal Investigator:Yoshiyuki Sakaki Ph.D. Phone: +81-3-5449-5622, Fax: +81-3-5449-5445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is conducted by Kitasato University JST sequencing
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                                                                                                                                                                                                                        /note="G51E05;The location is between each flanking site
of PCR primers."
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                                                                                      of PCR primers
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                     /note="379/630;The location is between each flanking site
                                                                                                                                       /standard_name="D21S370"
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Tel:81-42-778-9923, Fax:81-42-778-9924)

E. coli transposon insertion:The present data does not contain E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the insertion and genomic sequences experimentally, removed the insertion sequences, reconstituted the present data. The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).
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Homo sapiens 2,083,744bp genomic DMA of 21q22.1 (REGION: D218226-AML CLONE RANGE: 078C10-f32E9)
Published Only in DataBase (1999) In press
2 (bases 1 to 100000)
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/map="21q22.1"
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Hattori, M., Fujiyama, Â., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishii, K., Totoki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Tudiden, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shintzu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K.,
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                                                                                                                                                                                                                                                                                                                                                                                 Nature 405 (6784), 311-319 (2000)
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Query Match
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                                                       12330 CGGCCGAGCCGAATCCCCTCCACCGGGACGCCCCGCTGCTCGGGAAGAGGCGGGCCC 12389
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                                                                          601 gagoggggccccggccgcgacctgagccgccgccgagcgcccgggggccatgcgacgacg 660
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661 ctgctgtggtcgctgctgctgctcggagtcttcgccgccgccgccgccgccgccgcca 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.5%; Score 675.4; DB 9; Length 56188; Best Local Similarity 99.7%; Pred. No. 1.7e-107; Matches 687; Conservative 0; Mismatches 1; Indels 1;
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                                                                                                                                                                                                                                                                                                               31459 AGGATGACGTCTGGGACTCTGTGTCCATTATCTCGGTTTCCGGAAAAGGAGCAAGAAGATG 31518
                                                                                                                                                                                                                                                                                                                                                                                                                            31399 AGTATTTAAAAAGACCCAACTCAGCCCATCTTAGAGGCCCTTGGACAAGGACAGCTCACCAA 31458
                                                                                    31579 AGCCATCGGAGCTGCTAGAGTTCTGTCTGGACTTTCCAGAGACCAGTATTCCCTTTTGCT 31638
1706 agccatcggagctgctagagttctgtctggactttccagagaccagtattcccttttgct 1765
                                                                                                                                                                                                                                                                                                                                                            1586 aggatgacgtctgggactctgtgtccattatctcgtttccggaaaaggagcaagaagatg 1645
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Homo saptens 56,188bp genomic DNA of 21q22.1
Published Only in DataBase (1999) In press
(bases 1 to 56188)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/.Tel:81-42-778-9923, Fax:81-42-778-9924)
The sequence is a part of the data (ACCESSION NO. AP000174 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1
Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens DNA, clone:PACB5.
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/clone="PACB5"
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Primer B: AGCCAGCACCATGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Thomas Hudson
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                                                                                                                                                                                                                                                                                                                                                                            Email: thudson@genome.wi.mit.edu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GGCTTCTCTTAAACACTAAAAAGGCATGTAATTGCTTGTTAGCAAAATGGATATGACACA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACCAAAGCATGGGCCTAGCCCACTGGCTCCCTGGAAGAGATCAAGCCATCGGAGCTGCTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 24.3%;
Local Similarity 97.5%;
                                                                                                                                                                                              TGCATGTTTTTT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGACTTTGGCAAATGAGCCGGAGCCCCTTGGGCAGGTCACACAACCTGTCCCAGCGAGGG 420
                                       Sequence 961 from Patent W00200928. AX345890
                                                                                  AX345890
                     AX345890.1 GI:18493776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prepared with primer pairs derived from U05875 -- Unigene. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buffer:
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/map="756_7_6; 807_B_1; 872_B_5; 934_D_9; 968_G_2;
760_C_11; (897,900)_H_(9,10,12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
5721 G 5721
                                                                      5661 TIGTIGTGGTCGTTGTTGTTGTTCGGAGTTTTCGTCGTCGTCGTCGCGGTTTCGTTA 5720
                                                                                                                                                             5601 GAGCGGGGTTTCGGTCGCGATTTGAGTCGTCGTCGAGCGTTCGGGGGTTATGCGATCGACG 5660
                                                                                                                                                                                                                                             5541 TGCGCGTTTTGCGTTATGGCGGTTTGGGCGGCGACGTGAGCGGTTTCGCGGATTTC 5600
                                                                                                                                                                                                                                                                                                                                5481 CGGTCGAGTCGAATTTTTTTTATCGGGACGTTTCGTTGTTGTTCGGGAAGAGGCGGGTTT 5540
                                                                                                                                                                                                                                                                                                                                                                                                                    5361 GCGTGGGGTTTTCGCGTTGTAGTCGTAGAGGTTTTTTAGGGTCGCGGTTTTCGGAGCGGG 5420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5301 TTTCGCGGGGTTTTAGTTTTTAGGACGTTTCGGGAGGTTTCGCGTTTTGGGAGGTCGGTT 5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5241 GGTTTGGGTCGGGGGTTTCGCGGGGTTTTTTCGGAAGGATCGCGGTTTTCGAAGGTGGGCG 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5181 GTATTCGAGAGGAGTTGGGGGGGGGTTAGGAGGGGTGGGGGGTTTTAGGGAAAGTTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5121 TGGGGGTTATTAAAGTAAATATTTCGATTAAAGGGGCGAATTTTCGAATTGTGCGATTAA 5180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5061 ATTTCGTTTTAAAAAAAAGGGGAGGGGGGGGGGGGAGAGTTGAAAGTTTAATATGTATTT 5120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5001 GTTGATTGGAGGCGGAGGTTGTAGTGAGTCGAGATCGTTTTATTGTATTTTAGTTTTGGTG 5060
                                                                                                661 ctgctgtggtcgctgctgctgctcggagtcttcgccgccgccgccgcgcggccccggcca 720
                                                                                                                                                                                                                                                                       541 tgcgcgccctgcgctcgccatggcggtttgggcggcgacgtgagcggctccgcgggacccc 600
                                        721 g 721
                                                                                                                                                                                     601 gageggggeeceggegegectgageegeegeeggegeeggggeeatgegaeegaeeg 660
                                                                                                                                                                                                                                                                                                                                                                        481 cggccgagccgaatcccctccaccgggacgccccgctgccgctcgggaagaggcgggccc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                              361 gcgtggggtcccccgcgctgcagccgcagaggcccccccagggccgcggttcccggagcggg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 tcccgcggggctccagtctccaggacgttccgggaggctccgcgctctgggaggccggct 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 actccgtctcaaaaaaaaggggaggggggggggggagagttgaaagcttaatatgtactt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 961 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic construct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     artificial sequence.
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426 c 4312 g 8091 t
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S69336
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810 gagcaatagcacgaggcctgttgtctaccgagtgcagttttaaatacaccgacagtaaatg 869
                                                                                  192 GAACCCAAGGCTTCACCTGTACAATGATGAGCAGATTCTAACTTGGGAGCCGTCACCTTC 251
                                                                                                                                                                                     135 TGGGCTCGGTGCCGCG---GCGTCCTCGCCAGACTCGTTTTCCCAGCTTGCGGCCCCTCT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                              750 gcacccgaagattcgcctgtacaacgcagagcaggtcctgagttgggagccagtggccct 809
                                                                                                                                                                                                                 690 agtottogocgocgocgocgocgocogocagacoctotttoccagotgocogotocta 749
                                                                                                                                                                                                                                                                                                                             630 ccgccgagcgcccggggccatgcgaccgacgctgctgtggtggttgctgctgctgctgctcgg 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                  570 gggcggcgacgtgagcggctccgcggaccccgagcggggccccgggccgcgacctgagccg 629
                                                                                                                                                                                                                                                                                                                                                                                              15 GGCGGGCGCTCGGCTCGCCATGGCCGCTGCGGTGCGAGTCTGAGCGGCGTCCACCCCGCG 74
                                                                                                                                                                                                                                                                                        75 GTCCCGGGCCGGCCCATGCGGCCTTTGCCACTGTGGCTGCCGCTGCTGCTCTG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 145654] from the original journal article.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94170381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon gamma receptor beta subunit-type I transmembrane protein/IFN-gamma R species-specific cofactor [mice, early B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hemmi,S., Bohni,R., Stark,G., Di Marco,F. and Aguet,M. A novel member of the interferon receptor family complements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S69336.1 GI:545841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      functionality of the murine interferon gamma receptor in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp. early B cell line Y16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 (5), 803-810 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAPPNIPEQIEEYLKDPDQFILEVLDKDGSPKEDSWDSVSIISSPEKERDDVLQTP
3 359 c 330 g 282 t
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FHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKI
RPHGLLSNVSCHETTANASARLQQVILIPLGIFALLLGLTGACFTLFLKYQSRVKY#F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        species-specific cofactor; precursor; ; This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="interferon gamma receptor beta subunit"
/protein_id="AAB3015.1"
/db_xref="G1:545842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comes from Fig. 2A; IFN-gamma R beta chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="G1:545842"
/translation="MRPLPLWLPSLLLCGLGAAASSPDSFSQLAAPLNPRLHLYND#Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="interferon gamma receptor beta subunit, IFN-gamma
beta chain, IFN-gamma R species-specific cofactor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILTWEPSPSSNDPRPVVYQVEYSFIDGSWHRLLEPNCTDITETKCDLTGGGRLKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="type I transmembrane protein/IFN-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene≈"interferon gamma receptor beta subunit, IFN-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.5%;
65.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 357; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 452.8; DB 10; Length 1283; Pred. No. 6.5e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFN-gamma R species-specific cofactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1283 bp
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	CTCCAAACACCGTGAACCAGGCCAG	1074	дb
	tgttctccaaacgctttgaaccaaagcatgggcctagc 1681	1644	Qy
1073	GAAGGAGGACTCCGGGGACTCCGTGTCAATTATTTCTTCTCCAGAAAAGGAGCGAGAA	1014	Дb
1643	aaaggatgacgtctgggactctgtgtccattatctcgttttccggaaaaggagcaagaaga	1584	Qy
1013	AGTATCTAAAGGACCCAGACCAATTCATCTTAGAGGTCTTGGACAAGGACGGTTCAC	954	ф
1583	agagtatttaaaagacccaactcagcccatcttagaggccttggacaaggacagctcacc	1524	Qy
953	AGCCGAGTGAAGTACTGGTTTCAGGCTCCGCCAAACATCCCGGAACAATCGA	894	ф
1523	tatagaggcctgattaaatactggtttcacactccaccaagcatcccattacagataga	1464	Qy
893	GCATCTTCGCATTGCTCGGCCTGACGGCGCCTGCTTCACCCTGTTCCTCAA	834	ф
1463	cgtgggaacattttcgttgctgtcggtgctggcaggagcctgtttcttcctggtcctgaa	1404	Qy
833	TCCTGTCACGAAACAGCAAATGCCTCCGCCAGGCTGCAGCAAGTCATCCTGATTCC	774	Ъ
1403	ctacgaaacaatggcagatgcctccactgagcttcagcaagtcatcctgatctc	1344	Qy
773	accacaré de crité de caarer	714	망
1343	ccaggcacaactgctttggaacaaagtaacatctttagagtcgggcatttaagcaacat	1284	· 0y
713	AAAC	654	Db
1283	agcaactccatttcattggataacttaaaaccctccagagtgtactgtttacaagt	1224	Qy
653	AGGAACAGGTTGAAGGCCCTTT	594	Db
1223	tatgtccattactgggaaaaaggaggaatccaacaggtcaaaggcccttt	1170	Qy
593	CACGGGGCAACTTTCA	540	Db
1169	tacetecaeggeetttttttg	1110	Qy
539	AAGGTTC	480	Db
1109	tatcggaatgtgactgtcgggcctccagaaaacattgaggtgaccccaggaagaggctc	1050	Qy
479	PAAGCGAGGGAACCTCACTTCCAAGTGGGTGGGGCCTGGAGCCATTTCAACA	420	Дb
1049	cattctgcctgggtgacaatgccttggtttcaaca	990	Qy
419	GGAGGCGGCTTGAAGCTTTTCCCACACCCATTCACAGTCTTCCTGCG	360	В
989	tggatttcaatgtcactctacg	930	Qy
359		312	В
929	ttcacggccgacatcatgtccatagggtgaattgtacacagatcacagcaacagagtg	870	Qy
311	CAGCAATGACCCAAGACCAGTGGTCTACCAGGTGGAATATAGCTTCATCGATGGCTCTTG	252	B

Search completed: September 10, 2002, 18:51:05 Job time: 7255 sec

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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                and is derived by analysis of the total score distribution.
                                                                                                                      2193.4
2185.6
1537.8
1173.8
1173.8
                                                                                                                                                                                                                                                                                                         Score
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      99.1
98.7
69.5
53.0
49.3
22.3
22.1
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7: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:
87: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:
87: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA198.DAT:
9: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA198.DAT:
9: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA198.DAT:
10: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
11: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
12: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
13: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
14: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
15: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
16: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
17: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
18: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
18: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT:
19: /SIDSI/gcgdata/
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Listing first 45 summaries
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2214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gttgactggaggcggaggtt.....ttgtatagtgcatgtttttt 2214
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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                                                            ABL32988
                                                                                                AAZ20505
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                                                                                                                                                                                                                                                                                                Description
                            Human immune syste
Human secreted pro
                                                                                      DNAX interferon-li
                                                                                                                IFN-gamma receptor DNA encoding novel
IFN-gamma receptor
                                                                                                                                                                                Human IFN-gamma ac
                                                                                                                                                                                                                                   DNA encoding novel
                                                                                                                                                                                                      IFN-gamma ac
   PA XX DR DR DR DR PT
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AAS76801
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                                                      P-PSDB; ABG12614.
                                                                                   WPI; 2001-639362/73.
                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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38.	38.	38.	38.	38.	38.	38.	38.	38.	38.	38.	138.6	38.	38.	38.	38.	38.	38.	38.	38.	38.	38.	38.	38.	43.	99.		69.	69.	69.	369.4	369.4	369.4	69.	369.4	78.
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581	479	479	479	479	479	479	479	479	470	470	470	470	470	470	470	470	421	421	421	421	421	421	421	167	474	915	382	382	382	382	382	382	382	38	16994
22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	16	23	23	22	22	22	22	22	22	22	22	24
ABA63760	AAI00811	AAI32148	AAI10888	AAK26255	AAK00802	ABA22328	ABA52539	ABA42117	AAI00883	AAI32222	AAI10962	AAK26329	AAK00874	ABA22401	ABA52613	ABA42191	AAI00272	AAI31590	AAI10337	AAK25708	AAK00268	ABA21799	ABA51982	AAT20234	AAS66888	AAS76799	AAI00882	AAI32221	AAI10961	AAK26328	AAK00873	ABA22400	261	ABA42190	98
foetal liv		#834 used	#821	bone n	brain	#794 fc	foeta	breast	#874 used	#908 used	#895	bone r	brain	#867 fc	foetal	breast		#276 used	#270	bone n	brain exp	#265 fc	foetal liv	an qene si	encoding	ncodin	#873	#907 used	#894	bone m	brain exp	#866 fo	foetal l	breast	Human immune syst

ALIGNMENTS

ID AAS76801 standard; cDNA; 2215 BP.

XX
AC AAS76801;
XX
T 13-FEB-2002 (first entry)
XX
DT 13-FEB-2002 (first entry)
XX
DNA encoding novel human diagnostic protein #12605.
XX
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
Homo sapiens.
XX
W0200175067-A2.
XX
PN W0200175067-A2.
XX
11-OCT-2001.
XX
21-MAR-2001; 2001WO-US08631.
XX
31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0549167.
XX
YA
XX
(HYSE-) HYSEQ INC.
XX
Drmanac RT, Liu C, Tang YT;
XX
Drmanac RT, Liu C, Tang YT;
XX
PPSDB; ABG12614.
XX
New isolated polynucleotide and encoded polypeptides, useful in

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CC (II). (II) is useful for generating antibodies against it, detecting or c quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical can imaging of sites expressing (II). (I) and (II) are useful in medical considers involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in cC diagnostics, forensics, gene mapping, identification of mutations cC responsible for genetic disorders or other traits to assess biodiversity cand to produce other types of data and products dependent on DNA and CC anino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
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541 tgcgcgccctgcgctcgccatggcggtttgggcggcgacgtgagcggctccgcgggacccc 600
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                               1620 gtttccggaaaaggagcaagaagatgttctccaaacgctttgaaccaaagcatgggccta 1679
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                      Suppressing tumours in mammals with accessory factor 1 (AF-1) - for interferon gamma, specifically induction of class I HLA antigens, including use of AF-1 DNA in gene therapy
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Disclosure; Fig 21B; 114pp; English
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                                                                                            WPI; 1995-106679/14.
                                                                                                                                    Cook JR,
                                                                                                                                                                (UYNE-) UNIV NEW JERSEY.
                                                                                                                                                                                          20-AUG-1993;
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                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                             Interferon-gamma; AF-1; tumour; ss.
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                                                                                                                        Soh J;
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841 gtgcagtttaaatacaccgacagtaaatggttcacggccgacatcatgtccataggggtg 900
                  841 gtgcagtttaaatacaccgacagtaaatggttcacggccgacatcatgtccataggggtg 900
                                                                                             781 caggtcctgagttgggagccagtggccctgagcaatagcacgaggcctgttgtctaccga
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Pred. No. 0;
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4 cccggggccatgcgaccgacgctgctgtggtcgctgctgctgctgctcggagtcttcgcc 63

Matches 1561;

Conservative

Score 1537.8; Pred. No. 0; 0; Mismatches

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Indels

2; Gaps

Local Similarity

69.5%;

DB 16; Length 1566;

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                                                          The sequence is that of a cDNA clone encoding human interferon-gamma accessory factor-1. Incorporation of AF-1 into immune and tumour cells re-establishes normal function with elimination of malignant
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Sequence 1566 BP; 402 A; 398 C; 357 G; 409 T; 0 other;
                                                                                                                    Disclosure; Fig 21A; 114pp; English.
                                                                                                                                                 antigens, including use of AF-1 DNA in gene therapy
                                                                                                                                                                                                                             WPI; 1995-106679/14.
                                                                                                                                                                                                                                                                        Cook JR,
                                                                                                                                                                                                                                                                                                    (UYNE-) UNIV NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                               22-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon-gamma; AF-1; tumour; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ84697;
                              See also AAQ84698-9.
                                                                                                                                                                                                              P-PSDB; AAR/1035.
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Disclosure; Fig.4A; 86pp; English.
                                                               Novel interferon gamma receptor beta chain polypeptide - for
                                                                                                                P-PSDB; AAR75783
                                                                                                                                     WPI; 1995-224321/29.
                                                                                                                                                                                                                                                                                                          09-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                    07-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                         W09516036-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFN-gamma receptor beta-subunit cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ90809;
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                                                                                                                                                                            Aguet M,
                                                                                                                                                                                                                      (HEMM/) HEMMI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interferon-gamma receptor beta subunit; huIFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon-gamma-antagonist;
                                                                                                                                                                                                                                                                (AGUE/)
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                                                                                                                                                                                                                                                                AGUET M.
                                                                                                                                                                                                                                         BOEHNI R.
                                                                                                                                                                            Boehni R,
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                        1408 ggaacattttcgttgctgtcggtgctggcaggagcctgtttcttccttggtcctgaaatat 1467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA insert as probe. chromosome 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding the human IFN-gamma receptor beta-subunit was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated from a gtl1 cDNA library using a previously isolated mouse cDNA insert as probe. The human gene was mapped to
                                                                                        784 tgctacgatacaatggcagatgcctccactgagcttcagcaagtcatcctgatctccgtg
                                                                                                                                                                                  724 gcacaactgctttggaacaaaagtaacatctttagagtcgggcatttaagcaacatatct 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 cactatcggaatgtgactgtcgggcctccagaaaacattgaggtgaccccaggagaaggc 543
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ggaacattttcgttgctgtcggtgctggcaggagcctgtttcttcctggtcctgaaatat 903
                                                                                                                   tgctacgaaacaatggcagatgcctccactgagcttcagcaagtcatcctgatctccgtg 1407
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Pred. No. 1.1e-246;
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
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                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1144 ccatcggagctgctagagttctgtctggactttccagagaccagt 1188
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                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 2694; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #2694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS66890 standard; cDNA; 1781 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002 (first entry)
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1376 ctgagcttcagcaagtcatcctgatctccgtgggaacattttcgttgctgtcggtggtggtgg 1435
                                                                        1001 TCTTTAGAGTCGGGCATTTAAGCAACATATCTTGCTACGAAACAATGGCAGATGCCTCCA 942
                                                                                                     1316 totttagagtogggcatttaagcaacatatottgctacgaaacaatggcagatgcctcca 1375
                                                                                                                                                                                                                                                                    1121 GAGGAATCCAACAGGTCAAAGGCCCTTTCAGAAGCAACTCCATTTCATTGGATAACTTAA 1062
                                                                                                                                                                                                                                                                                              1196 gaggaatccaacaggtcaaaggccctttcagaagcaactccatttcattggataacttaa 1255
                                                                                                                                                                         1061 AACCCTCCAGAGTGTACTGTTTACAAGTCCAGGCACAACTGCTTTGGAACAAAAGTAACA 1002
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                                                                                                                                                                                                                                                                                                                                                                    1181 TTGACATCGCTGATACCTCCACGGCCTTTTTTTTGTTATTATGTCCATTACTGGGAAAAAG 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1241 CAGAAAACATTGAGGTGACCCCCAGGAGAAGGCTCCCCTCATCATCAGGTTCTCCTCTCCCT 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1301 ATTCTGCCTGGGTGACAATGCCTTGGTTTCAACACTATCGGAATGTGACTGTCGGGCCTC 1242
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1781 BP; 436 A; 428 C; 486 G; 430 T; 1 other;
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AAZ20505;

19-NOV-1999 (first entry)

DNAX interferon-like receptor subunit 2 coding sequence.

AAZ20505

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                                                                                        101 TACTCCTAGTAATTTACAAGATTTTGTTTTTAAACTTGAAATAATTGTATTTGTATAGTG
                                                                                                                                                                                    221 GAGCCGGGGACGCCCTTGGGCAGGTCGACACACCTGTCCCAGCGAGGGACACNCCGAGT 162
                                                                                                                                                                                                                                                                                                                                                                                        281 TATTGGTTGGGCTTGAGCAGTCCAGAAGACCCTGGTCGTCGTCCTTGACTTTGGCAAACT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 CATGTAATTCGCTTGTTACGCAAAATCGGATACGACACCTCTCTGAATACTTTTTTCAT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 ATTTTACGGGAGATATTCCCAGGAAAAATTAAGGCCTCCTCCTTAAACACCCTAAAAAGGC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 CCAAGCTTTTTCTATTTTTCCTTAAAGGAATTTTCCAAAAATCAAAATTCCCAGAATGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521 TCTAAAAAGGCCCTGTCCCTGCCAGACCATGAGAGAACGGCAGGTTCTCATGGGGGGGTGA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    581 TGCTAGAGGTTTCTGTTTTGGGACCTTTCCCAGAAGACCAGGTATTCCCCTTTTGCGGGCC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641 CCAAAAGCATGGGCCTAGCCCACTGGCTCCCCTGGAAAAAAGATCCAAGCCCATCGGAGGC 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         701 TGTGTCCATTATCCCGTTTCCGGAAAAGGAGCAAGAGGATGTTCTCCAAACGCTTTGTAA 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        821 CCCCTCCACCAAGGCATCCCATTTCCAGATAGAAGGAGTATTTTAAAAGACCCCAACTCAG
41 CATGTTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      881 CAGGAGCCCTGTTTCTTCCTGGTCCTGAAATATAGAGGCCTGGTTTAAATCCTGTTTTCC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          941 CTGAGCTTCAGCAAGTCATCCTGATCTCCGTGGGAACATTTTCGTTGCTGTCGGTGCTGG 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCATTCTTAGAGGCCTTTGGCCAAGGACAGCTCACCAAAGGGATGACGTCTTGGGACTC 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular development; cell differentiation; ss
                                                                                                                                                                                                                                                                                             1072 cctccagaaaacattgaggtgaccccaggagaaggctccctcatcatcaggttctcctct 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New receptor subunits potentially useful, e.g. for treating degenerative and abnormal conditions that involve cellular development,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNAX interferon-like receptor subunit; DIRS1; DIRS2; cytokine receptor;
                                                                                                                                                                                                                                                                                                                                                                    1012 ctccattctgcctgggtgacaatgccttggtttcaacactatcggaatgtgactgtcggg 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1244 BP; 324 A; 323 C; 281 G; 316 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 77-79; 82pp; English.
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                  1312 aacatctttagagtcgggcatttaagcaacatatcttgctacgaaacaatggcagatgcc 1371
                                                                                     1252 ttaaaaccctccagagtgtactgtttaccaagtccaggcacaactgctttggaacaaagt 1311
                                                                                                                                                         1192 aaaggaggaatccaacaggtcaaaggccctttcagaagcaactccatttcattggataac 1251
                                                                                                                                                                                                                                           1132 ccctttgacatcgctgatacctccacggccttttttttgttattatgtccattactgggaa 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that involve cellular development, differentiation or function
260 ttgagacccttaagagaatactgtttacaagtgaaggcgcatctctttcgcacatcctgc 319
                                                                                                                                        200 aaggcgggaatccaaaaggttaaaggtcctttcaagagcaactccatcgtgttggatggc 259
                                                                                                                                                                                                         143 cccttcgacgtccc---tcccaacctgggctatttccagtactatgtccattactgggaa 199
                                                                                                                                                                                                                                                                              23 ctggtttccccctggctgacagtgccttggttcctgtcctgttggaatgttaccattggg 82
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     844;
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                                                                                                                                                                                                                                                                                                                                                                                                                 22.3%; Score 494.4; DB 20; Length 1244; milarity 69.4%; Pred. No. 2.3e-98; Conservative 0; Mismatches 331; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moore KW, Murgolo NJ, Bazan JF;
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1612 attatctcgtttccggaaaaggagcaagaagatgttctccaaa-cgctttgaaccaaagc 1670
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                                                                                                   1197 ctataattaacttttt 1212
                                                                                                                                                                                                                                1137 gccctgtaaatagtttcacagagattaagcctttttttccccccaagttaggaataaaaga 1196
                                                                                                                                                                                                                                                                            2137 atottgtaaatatactoctagtaatttaagattttgtttttaaactggaaataaaagatt 2196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1844 --aaagaattttcaaa----atcaaattccagaatgattttacggagatatcccaggaaa 1897
                                                                                                                                                                 2197 gtatagtgcatgtttt 2212
                                                                                                                                                                                                                                                                                                                                                                     1080 gaagggacattaagtggcccttc---ttcatatccaaacacctggcttgaaatgtgatta 1136
                                                                                                                                                                                                                                                                                                                                                                                                      2077 cgagggacactgagtggcccttcatgtacatccatggtgtgtgctggcttaaaatgtaatta 2136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          979 ggcacgcctctgacactttttcg-----tcagcagccaggacacgaggtcc 1024
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ABL32988 standard; DNA; 16994 BP

ABL32988;

26-MAR-2002 (first entry)

Human immune system associated gene SEQ ID NO: 961.

Human; immune system disease; cytosine methylation; antiasthmatic;

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                                                       5301 tttcgcggggttttagtttttaggacgtttcgggaggtttcgcgttttgggaggtcggtt
                                                                                                                                                                                                        5181 gtattcgagagagagttgggggggttaggagggtgggggttttagggaaagttcggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                  5241 ggtttgggtcggggtttcgcggggttttttcggaaggatcgcggttttcgaaggtgggcg
                                                                                                                                                                                                                                                                                   5121 tgggggttattaaagtaaatatttcgattaaaggggcgaattttcgaattgtgcgattaa 5180
                                                                                                                                                                                                                                                                                                                                                                                                                                  5001 gttgattggaggcggaggttgtagtgagtcgagatcgttttattgtattttagtttggtg 5060
                                                                                                                                                                                                                                                                                                                                                             5061 atttcgttttaaaaaaaaggggaggggggggggggagagttgaaagtttaatatgtattt 5120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16994 BP; 4165 A; 426 C; 4312 G; 8091 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 961; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                       241 99cct999ccg999tctcgcg9ggcccttccggaaggatcgcggcccccgaaggtgggcg
                                                                                                                                                                                                                            181 gcacccgagagagagttgggggggtcaggagggtggggtccaggggaacgcccggg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute_myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
361 gegtggggtccccgcgctgcagccgcagaggcccccccaggggccgcgggttccccggagcggg
                                                                               301 tcccgcggggctccagtctccaggacgttccgggaggctccgcgctctgggaggccggct
                                                                                                                                                                                                                                                                                                       121 tgggggctattaaagcaaacatttcgactaaaggggggaatcctcgaattgtgcgatcaa 180
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79.9%;
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 16994; .8e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145;
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The invention relates to the isolation of genes AAF23894-F23935 encoding 42 human secreted proteins AAB59465-B59506. The genes can be used to generate fusion proteins by liking to the gene for the human immunoglobulin G Fc portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical
                                                                                                                             Claim 1; Page 414-415; 440pp; English.
                                                                                                                                                              Nucleic acids encoding 42 human secreted polypeptides, useful for preventing, diagnosing and/or treating immune, hyperproliferative cardiovascular and neurological disorders or infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF23929 standard; cDNA; 1233 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disease; infection; human; secreted protein; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1012 ctccattctgcctgggtgacaatgccttggtttcaacactatcggaatgtgactgtcggg 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1233 BP; 326 A; 319 C; 274 G; 314 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1431 gctggcaggagcctgtttcttcctggtcctgaaatatagaggcctgattaaatactggtt 1490
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                                   1727 tc-tgtctggactttccagagaccagtattcccttttgctgcctctaaaaggcctgtccc 1785
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ccatgtcagcactttatggaatccggtcctccattttcctgtccccaaaaggccgtcagt 788
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             P-PSDB; AAR75782
                                                                                                                                       09-DEC-1993;
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                         WPI; 1995-224321/29
                                                    Aguet M,
                                                                                                                                                                                                                                                                                                                                                                                         interferon-gamma-antagonist; ss.
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                                                                                                          (AGUE/) AGUET M.
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                                                                  1284 ccaggcacaactgctttggaacaaaagtaacatctttagagtcgggcatttaagcgaacat 1343
                                                                                                                                                            1224 cagaagcaactccatttcattggataacttaaaaccctccagagtgtactgtttacaagt 1283
                                                                                                                                                                                                                                                                 1170 ttattatgtccattactgggaaaaaggaggaatccaac----aggtcaaaggcccttt 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                       1050 ctatcggaatgtgactgtcgggcctccagaaaacattgaggtgaccccaggagaaggctc 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COSN 31 cells were transformed with pools of murine early beta-cell-derived cDNA library pAGS-3, and cells responsive to muIFN-gamma in terms of Tac antigen expression were enriched by panning. Isolated cDNA clones contained a common 1.1 kb insert, which was isolated and used to probe a mouse lambda-gtll cDNA library. A positive clone (lambda-.C19) was isolated which contained a 1283 bp EcoRI insert
1344 atcttgctacgaaacaatggcagatgcctccactgagcttcagcaagtcatcctgatctc 1403
                                                                                                                                                                                                                                                                                                                                                               1110 cctcatcatcaggttctcctctccctttgacatcgctgatacctccacggcctttttttg 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1283 BP; 312 A; 359 C; 330 G; 282 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig.2A; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage
                                          714 tgaggcacaactgattttgaaaaacaaaaaatccgaccacatgggctcttgagcaatgt 773
                                                                                                                                                                                                                         594 gtatcttgtccactactgggaaaagtcagaaacccaacaggaacaggttgaaggcccttt 653
                                                                                                                                                                                                                                                                                                                     540 cctcgtcatacacttctcccctccctttga-----tgtgttccacggggcaacttttca 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 tgacttaacaggaggcggccgcttgaagcttttcccacaccccattcacagtcttcctgcg 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AAQ90808) encoding IFN-gamma receptor beta-subunit
                                                                                                                                     654 caagagcaactccattgtgctgggcaatctgaagccatacagagtatattgtttacaaac 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990 ccttcgagctgagctgggagcactccattctgcctgggtgacaatgccttggtttcaaca 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 g-----cataggttgctggagccgaactgtacggacatcacagagacaaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   870 gttcacggccgacatcatgtccataggggtgaattgtacacagatcacagcaacagagtg 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 cagcaatgacccaagaccagtggtctaccaggtggaatatagcttcatcgatggctcttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            690 agtettegeegeegeegeegeegeeagaeeetettteeeagetgeeegeteetea 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  570 gggcggcgacgtgagcggctccgcggaccccgagcggggccccgggccgcgacctgagccg 629
                                                                                                                                                                                                                                                                                                                                                                                                            480 ctatgagaatgttactgttggacctccgaaaaacatctcggtgaccccaggaaaaggttc 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 gaacccaaggcttcacctgtacaatgatgagcagattctaacttgggagccgtcaccttc 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750 gcacccgaagattcgcctgtacaacgcagagcaggtcctgagttgggagccagtggccct 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 tgggctcggtgccgcg---gcgtcctcgccagactcgttttcccagcttgcggcccctct 191
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                                                                                                                               Claim 1; SEQ ID NO 962; 32pp + Sequence Listing; German.
                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL32989 standard; DNA; 16994 BP
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                                                                                                                                                                     cytosine methylation
                                                                                                                                                                                                                                       WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; as.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL32989;
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                                                                                                                                                                                                                                                                                                                                                             2000DE-1032529
                                                                                                                                                                                                                                                                         Berlin K;
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can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel

The present invention provides a number of human immune system associate

are modified by the methylation of cytosines.

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                                                                                                                                                                                                                                                                                                                                                                                                                        11753 ATCTAAACCGAAATCTCGCGAAACCCTTCCGAAAAAAATCGCGACCCCCGAAAATAAACGT 11694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11993 TTAACTAAAAACGAAAATTACAATAAACCGAAATCGCCCCACTACACTCCAACCTAATAA 11934
                                                                                                                                                                                      11273 A 11273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11693 CCCGCGAAACTCCAATCTCCAAAACGTTCCGAAAAACTCCGGCGCTCTAAAAAAACCGACTA 11634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11873 АЛАЛАСТАТТАЛАЛАСЛАЛСТТССВАСТАЛАЛАЛАССПССТССВАТТАТАССВАТСАЛА 11814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16994 BP; 4378 A; 426 C; 4139 G; 8051 T; 0 other;
Human; microarray; single exon probe; gene expression; breast;
                             Human breast cell single exon nucleic acid probe #885.
                                                        01-FEB-2002 (first entry)
                                                                                     ABA42190;
                                                                                                                 ABA42190 standard; DNA; 382 BP
                                                                                                                                                                                                                                                                                                                        182 cacccgagaggagagttggggggggtcaggaggggtgggggctccaggggaacgcccgggg 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 gggggctattaaagcaaacatttcgactaaaggggcgaatcctcgaattgtgcgatcaag 181
                                                                                                                                                                                                                                                                   662 tgctgttggttgctgctgctgctcggagtcttcgccgccgccgccgccgccgccgccgccag 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 cgtggggtccccgcgctgcagccgcagaggccccccagggccgcggttcccggagcggga 421
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                                                                                                                                                                                                                    722 a 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ctccgtctcaaaaaaaggggagggggggggggggagagttgaaagcttaatatgtacttt 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507;
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pred. No. 9.9e-73;
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 1989 tgggctgagcagtcagaagacctggtcgtcgtcttgactttggcaaatgagccggagccc 2048
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derived from many of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias concerns the production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1749 cagtattcccttttgctgcctctaaaaggcctgtccctgcagacatgagagacaggat 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                        Sequence 382 BP; 101 A; 82 C; 86 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 885; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast, comprises number of single exon nucleic acid probes
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                                    1929 tgtaattgcttgttagcaaaatggatatgacacatctctgatacttttttcattattggt 1988
                                                                                                                                                                                            1869 gaatgattttacggagatatcccaggaaaattaaggcttctctttaaacactaaaaaggca 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-496933/54.
180 tgtaattgcttgttagcaaaatggatatgacacatctctgatacttttttcattattggt 239
                                                                                                                                                        120 gaatgattttacggagatatcccaggaaaattaaggcttctcttaaacactaaaaaggca
                                                                                                                                                                                                                                                                                                    61 ctcatgggggtgacaagc-ttttttttttttttttcttaaagaattttcaaaatcaaattcca 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 cagtattcccttttgctgcctctaaaaggcctgtccctgcagacatgagagacagcaggt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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99.5%;

 Mismatches

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                                                                                                                                     Query Match
Best Local
                                                       1749 cagtattcccttttgctgcctctaaaaggcctgtccctgcagacatgagagacagcaggt 1808
       1809 ctcatggggtgacaagcttttttttttttttttcttaaagaattttcaaaatcaaattcca 1868
                                                                                                                                                                                                Sequence 382 BP; 101 A; 82 C; 86 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 917; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483447/52.
                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dire
                                                                                                                                                                                                                                                                                   probe of the invention.
                                                                                                                                                                                                                                                                                                measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                               liver. The single exon nucleic acid probes may be used for predicting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human foetal liver single exon nucleic acid probe #917.
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                                    1 cagtattcccttttgctgcctctaaaaggcctgtccctgcagacatgagagacagcaggt 60
                                                                                                                               Local Similarity
                                                                                                                                                                                                                               WIPO at ftp.wipo.int/pub/published_pct_sequences.
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2000US-0207456.
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2000US-0234687.
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                                                                                                                           16.7%;
99.5%;
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                                                                                                           Score 369.4; DB 22; Length 382; Pred. No. 3.1e-71; 0; Mismatches 1; Indels 1;
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
         The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                     Claim 1; SEQ ID No 866; 530pp; English.
                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #866 for gene expression analysis in human heart cell sample
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                                                                                                                                                                                                                                                                          Hanzel DK,
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                                                                                                                                                                                                                                                                          Chen W,
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Matches
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26-MAX-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
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                                                     04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                    epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                     microarray; Alzheimer's disease; multiple sclerosis; schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe SEQ ID NO: 864.
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe;
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                 (MOLE-) MOLECULAR DYNAMICS INC
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                                                     2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1749 cagtattccctttttgctgcctctaaaaggcctgtccctgcagacatgagagacagcaggt 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                     2109 catggtgtgctggcttaaaaatgt 2131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
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09-AUG-2001.
                                                                                                                        Human; bone marrow expressed exon; gene expression analysis;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                            06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                             AAK26328 standard; DNA; 382 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2049 cttgggcaggtcacacaacctgtcccagcgagggacactgagtggcccttcatgtacatc 2108
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                                                                                                                      microarray; cancer;
                                                                                                                                                                                  Human bone marrow expressed single exon probe SEQ ID NO: 885
                                        WO200157276-A2
                                                                                Homo sapiens.
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Local Similarity 99.5%;
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30-JAN-2001; 2001WO-US00668.

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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-023659.

04-OCT-2000; 2000GB-0024263.
                        2109 catggtgtgctggcttaaaatgt 2131
                                                                                                                                                                                1989 tgggctgagcagtcagaagacctggtcgtcgtcgtcttgactttggcaaatgagccggagccc 2048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 382 BP; 101 A; 82 C; 86 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the hun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 885; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow – \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the probes of the invention.
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                                                                                                                                                          240 tgggctgagcagtcagaagacctggtcgtcgtcttgactttggcaaatgagccggagccc 299
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360 catggtgtgctggcttaaaatgt 382
                                                                           300 cttgggcaggtcacacaacctgtcccagcgagggacaccgagtggcccttcatgtacatc
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Search completed: September 10, 2002, 19:05:32

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Run on:

OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Sequence 3, Application
Patent No. 6287853
GENERAL IMPORMATION:
APPLICANT: Pestka,
APPLICANT: KOCENKO,
APPLICANT: Soh, Jae
APPLICANT: Donnelly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-871-572B-3
; ANTI-SENSE:
US-08-871-572B-3
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                                                                                                                         TELEFAX: (908) 273-4679 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cook, Jeffrey
APPLICANT: Emmanuel, Stuart
APPLICANT: Schwartz, Barbara
TITLE OF INVENTION: Accessory Factor for Interferon Gamma
TITLE OF INVENTION: and Its Receptor
                                                                                                                                                    REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UND1-011
TELECOMMUNICATION : INFORMATION:
TELEPHONE: (908) 273-4988
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                         MOLECULE TYPE: HYPOTHETICAL:
                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2255 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Muccino, Richard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                   FILING DATE: 9-
CLASSIFICATION:
                                                      TOPOLOGY:
                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                 STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                   758 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soh, Jaemog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kotenko,
             NO
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                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                       Richard R. Muccino
                           NO
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3 US-09-206-537-7

4 US-09-430-854-7

4 US-09-103-840A-2

2 US-08-770-379-16

4 US-08-77-669A-16

4 US-09-230-371A-16

4 US-07-945-283-1

5 PCT-US91-06532-1

5 PCT-US91-06535-5

4 US-08-765-907A-1
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US-08-284-941-1

US-08-447-642-1

US-09-236-503-1

PCT-US93-02147A-1

US-08-785-420-1
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Sequence 16, Appl
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Sequence 5, Appli
Sequence 1, Appli
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Sequence: Database : Post-processing: Minimum Match 0% Total number of hits satisfying chosen parameters: Scoring table: Perfect score: o.υ.+. ω.ν.+. September 10, 2002, 16:52:50; Search time 181.1 Seconds (without alignments) 3002.941 Million cell updates/sec Issued_Patents_NA:* Gapop 10.0 , Gapext 1.0 IDENTITY_NUC US-09-843-377-3 Listing first 45 summaries 383533 seqs, 122816752 residues 1 gttgactggaggcggaggtt.....ttgtatagtgcatgtttttt 2214 Maximum Match 100% /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/Dackfiles1.seq:*

and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

SUMMARIES

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US-08-4-88-568A-11 US-07-945-283-1 US-08-483-533-37 US-09-283-471A-37	-08-804 -08-690 -09-259 -08-843	969-69	-09-165-264-8 -09-165-264-7 -09-165-264-1 -08-690-473-1 -09-259-821A- -08-843-659-1 -08-458-568A-	US-08-871-572B-3 US-08-871-572B-2 PCT-US94-14277-7 PCT-US94-14277-1 US-09-128-155-16 US-08-406-030A-3	ID
Sequence 11, Appl Sequence 1, Appli Sequence 37, Appl Sequence 37, Appl	:++++	Sequence 14, Appl Sequence 13, Appl Sequence 12, Appl Sequence 1, Appli Sequence 7, Appli	8, A 7, A 11, A 1, A	Sequence 3, Appli Sequence 2, Appli Sequence 7, Appli Sequence 1, Appli Sequence 16, Appli Sequence 3, Appli	Description

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (908) 273-46 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
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LENGTH: 1566 base pairs
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Accessory Factor for Interferon Gamma TITLE OF INVENTION: and Its Receptor NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Muccino, Richard R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2161 AATTTAAGATTTTGTTTTTAAACTGGAAATAAAAGATTGTATAGTGCATGTTTTTT 2216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2159 aatttaagattttgtttttaaactggaaataaaagattgtatagtgcatgtttttt 2214
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                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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  760 attogoctgtacaacgcagagcaggtcctgagttgggagccagtgggccctgagcaatagc 819
                                                           APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pain-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/871,572B FILING DATE: 9-JUNE-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,538
                                                                                                                                      4 CCCGGGGCCATGCGACGACGCTGCTGCTGGTCGCTGCTGCTGCTCGGAGTCTTCGCC 63
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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Schwartz, Barbara
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ON: 435
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                                                                                                                                                                                                            69.5%; Score 1537.8; DB 4; Length 1566; 99.7%; Pred. No. 0; ative 0; Mismatches 2; Indels 2;
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                                                                                           1720 ctagagttctgtctggactttccagagaccagtattccctttttgctgcctctaaaaggcc 1779
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                                                                       1480 aaatactggtttcacactccaccaagcatcccattacagatagaagagtatttaaaagac 1539
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                                                               ; TOPOLOGY: linear PCT-US94-14277-7
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Best Local Similarity
                 Query Match
                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1900 taaggettetettaaacaetaaaaaggeatgtaattgettgttagcaaaatggatatgae 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1960 acatototgatacttttttcattattggttgggctgagcagtcagaagacctggtcgtcg 2019
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                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1197 bases
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                             Love
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460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                          patin (Genentech)
                                                                                                                                                                                                                                                                             Richard B
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53.0%;
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Score 1173.8; DB 5; Pred. No. 6.7e-266;
               Length 1197;
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Matches 1178; Conservative
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1024 GATGAGCTCTGGGACTCTGTGTCCATTATCTCGTTTCCGGAAAAGGAGCAAGAAGATGTT 1083
                                                                                                                                                                              1528 tatttaaaagacocaactcagoccatcttagaggocttggacaaggacaggtcaccaaag 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1288 gcacaactgctttggaacaaaagtaacatctttagagtcgggcatttaagcaacatatct 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   568 ttgggcggcgacgtgagcggctccgcgggaccccgagcggggccccgggccgcgacctgagc 627
                                                                                                                                                                                                                                                                                                                                                                                                                            844 GGAACATTTTCGTTGCTGCTGGTGCTGGCAGGAGCCTGTTTCTTCCTGGTCCTGAAATAT 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    784 TGCTACGATACAATGGCAGATGCCTCCACTGAGCTTCAGCAAGTCATCCTGATCTCCGTG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664 AGCAACTCCATTTCATTGGATAACTTAAAACCCTCCAGAGTGTACTGTTTACAAGTCCAG 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 CGCCTTCGAGCTGAGCTGGGAGCACTCCATTCTGCCTGGGTGACAATGCCTTGGTTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  748 cagcacccgaagattcgcctgtacaacgcagagcaggtcctgagttgggagccagtggcc 807
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                                                                                                                                            964 TATTTAAAAGACCCAACTCAGCCCATCTTAGAGGCCCTTGGACAAGGACAGCTCACCAAAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 TGTGACTTCACTGCCGCCAGTCCCTCAGCAGGCTTCCCAATGGATTTCAATGTCACTCTA 423
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                                     gatgacgtctgggactctgtgtccattatctcgttttccggaaaaggagcaagaagatgtt 1647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTATTATGTCCATTACTGGGAAAAAGGAGGAATCCAACAGGTCAAAGGCCCCTTTCAGA 663
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PCT-US94-14277-1
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                                                                                                                                                                                                                                                                                                                                                                 Matches 734; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aguet, Michel APPLICANT: Bohni, Ruth APPLICANT: Hemmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1144 CCATCGGAGCTGCTAGAGTTCTGTCTGGACTTTCCAGAGACCAGT 1188
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LENGTH: 1283 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1708 ccatcggagctgctagagttctgtctggactttccagagaccagt 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
750 gcacccgaagattcgcctgtacaacgcagagcaggtcctgagttgggagccagtggccct 809
                                                                                                                                                                                                630 ccgccgagcgcccggggccatgcgaccgacgctgctgtggtcgctgctgctgctgctgctcgg 689
                                                                                                                                                                                                                                                                                                         570 gggcggcgacgtgagcggctccgcggaccccgagcgggccccggccgcgacctgagccg 629
                                                                          135 TGGGCTCGGTGCCGCG----GCGTCCTCGCCAGACTCGTTTTCCCAGCTTGCGGCCCCCTCT 191
                                                                                                      690 agtottogocgocgocgoggococgocagacoctottttococagotgocogotoctoa 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    75 GTCCCGGGCCGGGCCATGCGGCCTTTGCCACTGTGGCTGCCGTCGCTGCTGCTCTG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415/952-98
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REGISTRATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         20.5%; Score 452.8; DB 5; Length 1283; 65.7%; Pred. No. 5.5e-97; 1tive 0; Mismatches 357; Indels 27; Gaps
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                                                                                              GENERAL INFORMATION: APPLICANT: Pan, Yan
                                                                                                                                          Sequence 16, Application US/09128155
Patent No. 6117654
     CURRENT APPLICATION NUMBER: US/09/128,155
                       APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                              1644 tgttctccaaacgctttgaaccaaagcatgggcctagc 1681
                                                                                                                                                                                                                                                                                                                                                                                                             1584 aaaggatgacgtctgggactctgtgtccattatctcgttttccggaaaaaggaagcaagaaga 1643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1224 cagaagcaactccatttcattggataacttaaaaccctccagagtgtactgtttacaagt 1283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540 CCTCGTCATACACTTCTCCCCTTCGCTTTGA-----TGTGTTCCACGGGGCAACTTTTCA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954 AGAGTATCTAAAAGGACCCAGACCAATTCATCTTAGAGGTCTTGGACAAGGACGGTTCACC 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894 ATACCAAAGCCGAGTGAAGTACTGGTTTCAGGCTCCGCCAAACATCCCGGAACAAATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     834 GTTGGGCATCTTCGCATTGCTGCTCGGCCTGACGGGCGCCTGCTTCACCCTGTTCCTCAA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774 ATCCTGTCACGAAACAACAGCAAATGCCTCCGCCAGGCTGCAGCAAGTCATCCTGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         714 TGAGGCACAACTGATTTTGAAAAAACAAAAAAATCCGACCACATGGGCTCTTGAGCAATGT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     654 CAAGAGCAACTCCATTGTGCTGGGCAATCTGAAGCCATACAGAGTATATTGTTTACAAAC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 GTATCTTGTCCACTACTGGGAAAAGTCAGAAACCCCAACAGGAACAGGTTGAAGGCCCTTT 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 CTATGAGAATGTTACTGTTGGACCTCCGAAAAACATCTCGGTGACCCCAGGAAAAGGTTC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810 gagcaatagcacgaggcctgttgtctaccgagtgcagtttaaatacaccgacagtaaatg 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990 ccttcgagctgagctgggagcactccattctgcctgggtgacaatgccttggtttcaaca 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TGACTTAACAGGAGGCGGCCGCTTGAAGCTTTTCCCACACCCCATTCACAGTCTTCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930 tgacttcactgccgccagtccctcagcaggcttcccaatggatttcaatgtcactctacg 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 G-----CATAGGTTGCTGGAGCCGAACTGTACGGACATCACAGAGACAAAGTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        870 gttcacggccgacatcatgtccataggggtgaattgtacacagatcacagcaacagagtg 929
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EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22120 GTCGGCTGCGGGGGGGGGGGGGGGGGGGTCGGGGTGG-GGGGTGCGTGTGGGCCGGGT 22062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Hauge, Brian M.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: Protein Production and Delivery
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496 ccctccaccgggacgccccgctgccgctcgggaagaggcggg 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 gtctccaggacgttccgggaggctccgcgctctgggaggccggctgcgtggggtccccgc 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 gttggggggggtcaggagggtggggctccagggaacgcccgggggcctgggccggggt 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 gctgcagccgcagaggccccccagggccgcggttcccggagcgggaaagtcccgcgcggg 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 ctcgcggggcccttccggaaggatcgcggcccccgaaggtgggcgtcccgcgggggctcca 315
                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                  STREET:
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Local Similarity 51.8%;
APPLICATION NUMBER: US/08/406,030A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 02-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 05-NOV-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 13-MAY-1
2329 TICGCGTCA 2321
                                                                                2563 GTCAGCGCCGGCCGGCGCGCTCCTCCCGGCCGCTCCTCCCGCCCGGCCCGGCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                2503 CCGACTCTGCGGCCGGCCCGACGAGCCCCTCG-----CGGGCACTGCCCCGGCCCCGGCCC 2449
                                                                                                                                                                                                                                                                                                                                                                                                                2623 CGCGGGGCATAAAACGGGCCGGAGCCGGCCCCGGGGCAGTAGAGCCGCGTACGGCCCGG 2564
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                                      744 tecteagea 752
                                                                                                         684 gctcggagtcttcgccgccgccgcggcgccccgccagaccctctttcccaagctgcccgc 743
                                                                                                                                                                                                    624 gagccgccgccgagcgcccggggccatgcgaccgacgctgctgtggtcgctgctgctgct 683
                                                                                                                                                                                                                                                                                   564 cggtttgggcggcgacgtgagcggctccgcggaccccgagcggggcccccggccgcgacct 623
                                                                                                                                                                                                                                                                                                                                                                   504 cgggacgccccgctgccgctcgggaagaggcgggccctgcgccctgcgccctgcgctacgccatgg 563
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 10-JUI
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LENGTH: 319
TYPE: DNA
    Query Match 2.8%; Score 62.8; DB 4; Length 320; Best Local Similarity 50.3%; Pred. No. 7.2e-06; Matches 154; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                        SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09165264 Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09165264 Patent No. 6197510
                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                              APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTION: Multi-Loci Genomic FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTION: Multi-Loci Genomic Analysis FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
                                                                                                              FEATURE:
                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                              TYPE: DNA
                                                                                                                                                           ENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    303 tgcagcaccctatc 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 ggtccccgcgctgcagccgcagaggccccccagggccgcggttcccggagcgggaaagtc 426
                                                                                                                                                                                                                                                                                                                                                                                                                                  487 agccgaatcccctc 500
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   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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489 ccgaat 494
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-11
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                                                                                                                                                                                                                                                                                                                                                                                        Matches 154; Conservative
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CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vinayage
TITLE OF INVENTION:
FILE REFERENCE: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                        189 gaggagagttggggggggtcaggagggtgggggctccaggggaacgcccggggggcctggg 248
369 tccccgcgctgcagccgcagaggccccccagggccgcggttcccggagcgggaaagtccc 428
                                                                                                                                                      309 ggctccagtctccaggacgttccgggaggctccgcgctctgggaggccggctgcgtggggg 368
                                                                                                                                                                                                                                                               249 ccggggtctcgcgggggcccttccggaaggatcgcgggcccccgaaggtgggcgtcccgcgg 308
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                                                                                                                                                                                                                            Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
TYPE: nucleac acid
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Best Local Similarity 49.1%;
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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    2250 GCGGTTCGTGCGCGACGCGCTGGTGCTCATGC-GCCTGCGCGGGGACCTGCGCGTGGCCG 2308
                                                                                  2190 CGCTTCCCCGCCGCCGCACGCCGACGCCCCCCCCGCCTGCGCGTGGCTGCGCGAGCT 2249
                                                                                                                                                                2072 CCTGC--CGCGGGATCCTGGAGGCGCTGGCCGAGGGCTTCGACGGCGACCTGGCGGCCGT 2129
                                                                                                                                                                                                                                                                                                                          2012 CCGACGACGACGCCGGCCGCCCCAGGCCGGCCGTGGCCGTCGAGTGCCTGGCCG 2071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         235 cccgggggcctggggccggggtctcgcggggcccttccggaaggatcgcggcccccgaagg 294
                                    533 gegggeeetgegeeetgegetegeeatggeggtttgggeggegaegtgageggeteeg 592
                                                                                                                  473 ggcgcgggcgggccgagccgaatcccctccaccgggacgccccgctgccgctcgggaagag 532
                                                                                                                                                                                              355 ccggctgcgtggggtccccgcgctgcagcgcagaggcccccccagggccgcgggttcccgg 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Highlander, Steven L
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Roizman, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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SEQ ID NO 1
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Best Local Similarity 49.1%;
Matches 250; Conservative
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CURRENT APPLICATION NUMBER: US/09/259,821A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROIZMAN, BERNARD TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: HERPES VIRUS, TYPE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2130 cccggggctggccgggcccggccagccccccgcgggcggagggacccgcggggcc 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1952 ccgccgcgcccgcctcccccgcgggggggcgacgaccccgacgccgccgccacgccgacg 2011
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                                                                                                                                                                                                                                                                                                                                                                            2190 cgcttccccgccgccgccgcacgccgacgcgccccgcctgcgcgcgtggctgcgcgagct 2249
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                                                    2369 gccccgcgctgccgcgggacccgcgcctgccgagctccgcggcggccgccgccgccgcggacc 2428
                                                                                                                                                             2309 gcggcagcgaggccgccgtggccgcgtgcgcgtgagcctggtcgccggggccctgg 2368
                                                                                                                                                                                                                                                                      2250 gcggttcgtgcgcgacgcgctggtgctcatgc-gcctgcgcgggggacctgcgcgtggccg 2308
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713 ccccgccagaccctctttcccagctgccc 741
                                                                                                                                                                                             593 cggaccccgagcggggccccggcggcgacctgagccgccgagcgcccgggggccatgc 652
                                                                                                                                                                                                                                                                                                      533 gcgggccctgcgcgccctgcgctcgccatggcggtttgggcggcgacgtgagcggctccg 592
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                                                                                                        653 gaccgacgctgctgtggtcgctgctgctgctgctcggagtcttcgccgccgccgccgcggg 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62.6; DB 4; Length 4257; Pred. No. 2.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
2250 GCGGTTCGTGCGCGACGCGCTGGTGCTCATGC-GCCTGCGCGGGGACCTGCGCGTGGCCG 2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2072 CCTGC--CGCGGGATCCTGGAGGCCTGGCCGAGGGCTTCGACGGCGACCTGGCGGCCGT 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1952 CCGCCGCGCCCCCCCCCCGCGGGGGGGGGGGCGACGCCCGACGCCGACGCCGACGCCACGCCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                       2130 CCCGGGGCTGGCCGGGGCCCGGCCAGCCCCCGCGGGCCGGAGGGACCCCGCGGGCCC 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2012 CCGACGACGACGCCGGGCGCGGGCCCAGGCCGGCCGTGGCCGTCGAGTGCCTGGCCG 2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                     533 gcgggccctgcgccctgcgctcgccatggcggtttgggcggcgacgtgagcggctccg 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 ccggctgcgtggggtccccgcgctgcagccgcagaggcccccccagggccgcggttcccgg 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 tgggcgtcccgcggggctccagtctccaggacgttccgggaggctccgcgctctgggagg 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 cccgggggcctgggccggggtctcgcggggcccttccgggaaggatcgcgggcccccggaagg 294
                                                                                                                                                                                                                                                      473 ggcgcgggcggccgagccgaatcccctccaccgggacgccccgctgccgctcgggaagag 532
                                                                                                                                                                                                                                                                                                                                                                                                                         415 адсядувавантссся сдедед детем -- трусстений председ пред председ председ председ председ председ председ председ председ председ п
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/843,659 FILING DATE: Concurrently Herewit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME:
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ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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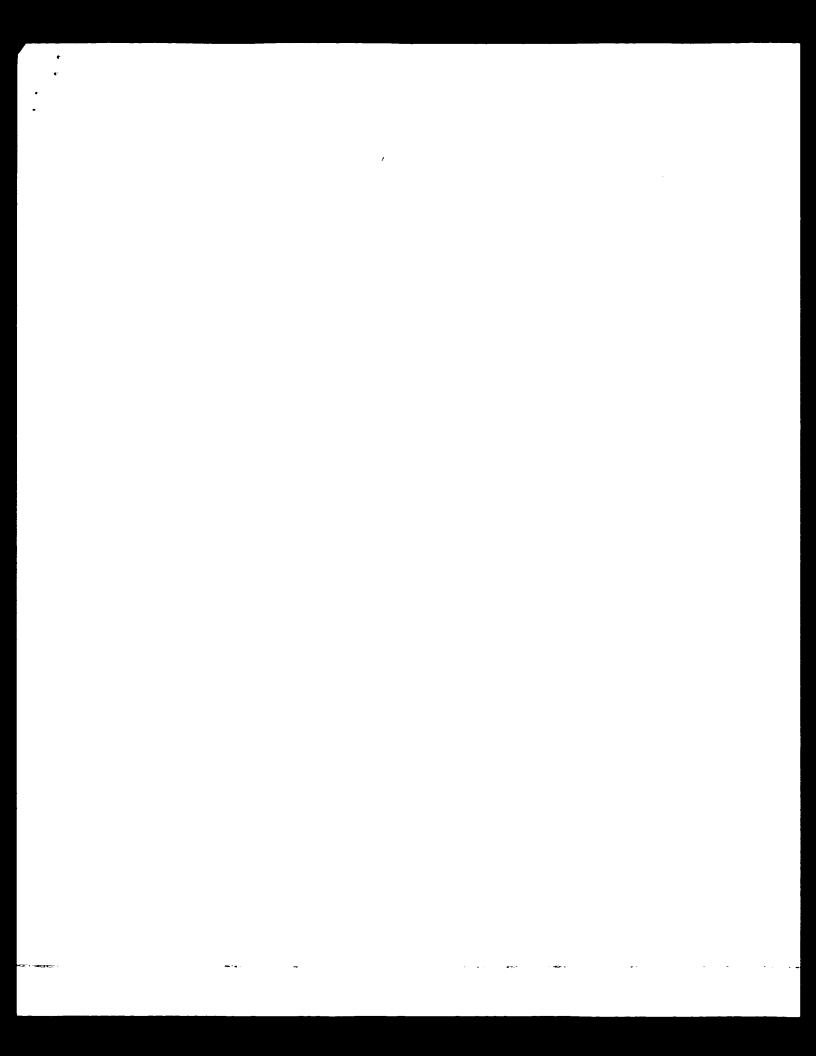
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                                                                                 Matches 250; Conservative
                                                                                                Query Match 2.8%;
Best Local Similarity 49.1%;
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeb, Lily
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2429 TGCTGTTTGACAACCAGAGCCTGCGCCCC 2457
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                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                            235 cccgggggcctgggccggggtctcgggggcccttccggaaggatcgcgggccccgaagg 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                 ORGANISM: Herpes Simplex Virus Type 1
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Liberty CITY: Philadelphia
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Leary Ph.D., Kathryn R. REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                 0; Mismatches 254; Indels
                                                                                                Score 62.6; DB 1;
Pred. No. 3.6e-05;
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US-09-165-264-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09165264 Patent No. 6197510 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/165,264 CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4424 GCGGTTCGTGCGCGACGCGCTGGTGCTCATGC-GCCTGCGCGGGGACCTGCGCGTGGCCG 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4484 CGCTTCCCCGCCGCCGCCGCACGCCGACGCGCCCCGCCTGCGCGCGTGGCTGCGCGAGCT 4425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4365 GCGGCAGCGAGGCCGCCGTGGCCGCCGTGCGCCGTGAGCCTGGTCGCCGGGGCCCTGG 4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4544 CCCGGGGCTGGCCGGGCCCGGCCAGCCCCCGCGGCCGGAGGGACCCGCGGGCCC 4485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4602 CCTGC--CGCGGGATCCTGGAGGCGCTGGCCGAGGGCTTCGACGGCGACCTGGCGGCCGT 4545
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                                                                                                                                                                                                                                                                                         713 ccccgccagaccctctttcccagctgccc 741
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                                          367 ggtccccgcgctgcagccgcagaggcccccccagggccgcggttcccggagcgggaaagtc 426
                                                                                                                           307 ggggctccagtctccaggacgttccgggaggctccgcgctctgggaggccggctgcgtgg 366
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Similarity 50.3%;
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VENTION: Multi-Loci Genomic Analysis
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US-09-165-264-13
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LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                         Matches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Multi-Loci Genomic Analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                          Local Similarity 50.3%;
                                                                                                                                             ggtccccgcgctgcagccgcagaggccccccagggccgcggttcccggagcgggaaagtc 426
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Pred. No. 1.1e-05;
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Job time: 6907 sec Search completed: September 10, 2002, 18:47:57 0



Scoring table:

AL574366 AL574366 AL572349 AL572349 BE796743 601587367 BM450234 AGENCOURT B1836121 603085823 BG750357 602709178 A1870491 w174c07, x

AL550338 AL550338 .

BI918514 603176688

EST 16-FEB-2001

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AI567425 tn38b03.x

BG756460 60271579

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AL576459 AL576459
AL563821 AL563821
AL571353 AL571353
AL553183 AL553183
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AL553184 AL542174
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AL528494 AL528494
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AL560745 AL560745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL550285 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI039YC04 5
                                                                                                                                                                                                                                                                                           Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         AL550285.1 GI:12887110
                                                                                                                                                                                                                                                                               Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                     vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                      /tissue_type="placenta"
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
                   Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" a 311 c 257 g 248 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1035)
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1 217 c 232 g 288 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies.
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/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Matches 1002; Conservative
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                                                                                                                                         445 CCMGTATTCCCTTTTGCTGCCTCTAAAAGGCCTGTCCCCGCAAACATTAGAAACAGCAGG
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Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
a 213 c 238 g 278 t 19 others
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/clone="CS0DD008YG20"
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TITLE
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                    1928 atgtaattgcttgttagcaaaatggatatgacacatctctgatacttttttcattattgg 1987
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L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="placenta" //tissue_type="placenta" f; Site_1: NotI; Ist strand cDNA /note="Vector: pcMVSPORT f; Site_1: NotI; Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT f vector. Library was normalized. Library was constructed by vector. Library was normalized.
                                                                                                                                                                                                                                                           http://fulllength.invitrogen.com"
235 c 266 g 287 t 1
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AL553183 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI073YF14 3
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                   1571 aggacagotcaccaaaggatgacgtctgggactctgtgtgtccattatctcgttttccggaaa 1630
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AGGACAGCTCACCAAAGGATGACGTCTGGGACTCTGTGTCCATTATCTCGGTTTCCGGAAA 527
                                                                                                                                                                                                                                                                                                                               tcatcctgatctccgtgggaacattttcgttgctgtcggtgctggcaggagcctgtttct 1450
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                                                                                                CATTACAGATAGAAGAGTATTTAAAAAGACCCAACTCAGCCCATCTTAGAGGCCCTTGGACA 587
                                                                                                                                            cattacagatagaagagtatttaaaagacccaactcagcccatcttagaggccttggaca 1570
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                                                                                                                                                                                                                                                                                                       TCATCCTGATCTCCGTGGGAACATTTTCGTTGCTGTCGGTGCTGGCAGGAGCCTGTTTC- 704
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
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                                                                                                                                                                                                                                                                                                                                                      Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
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CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockvil, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                  /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
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/lab_host="DH10B"
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1188 ggaaaaaggaaggaatccaacaggtcaaaggccctttcagaagcaactccatttcattgga 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                            1368 tgcctccactgagcttcagcaagtcatcctgatctccgtgggaacattttcgttgctgtc 1427
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1548 gcccatcttagaggccttggacaaggacagctcaccaaaggatgacgtctgggactctgt 1607
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                                                                                  676 GTTTCACACTCCACCAAGCATCCCATTACAGATAGAAGAGTATTTAAAAAGACCCAACTCA 617
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                                                                                                                                                                                                                                  GGTGCTGGCAGGAGCCTGTTTC-TCCTGGTCCTGAAATATAGAGGCCTGATTAAATACTG 677
                                                                                                                                                                                                                                                                                                                                                                                   TGCCTCCACTGAGCTTCAGCAAGTCATCCTGATCTCCGTGGGAACATTTTCGTTGCTGTC 736
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Email: seqref@genoscope.cns.fr,
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1 207 c 224 g 280 t 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end enriched, double-stranded cDNA was digested with Not,I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 TTGGCAAATGAGCCGGAGCCCCTTGGGCAGGTCACACAACVTGTCCCAGCGAGGGACAST 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 AATTKTCAAAATVAAATTCCAGAATGATTTTACGGAGATATCCCAGGAAAATTAAGGCKT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 CAGACATGAGARACAGCAGGTCTCATGGGGSCVACAAGC--TTTTTTTTTTTTTTTTAAAG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 CTGTCTGGACTTTCCAGAGACCAGTATTCCCTTTTGCTGCCTCTAAAAAGGCCTGTCCCTG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               556 GTCCATTATCTCGGTTTCCGGAAAAGGAGCAAGAAGATGTTCTCCAAACGCTTTGAACCAA 497
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                                                                                                                                                                                                           Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1013)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                                                                                                                                                                                                                                                                                                                                                              AL528494 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC029YK17 5
                                                                                                                                                                             Genoscope - Centre National de Sequencage
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                                                                                                                                       91006 EVRY cedex - France segref denoscope.cns.fr. web : www.genoscope.cns.fr.
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                            /clone="CS0DC029YK17"
/clone_lib="LTI_NFL003_NBC3"
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                              location/Qualifiers
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Matches 940;
1354 gaaacaatggcagatgcctccactgagcttcagcaagtcatcctgatctccgtgggaaca 1413
                                                                                                                1294 ctgctttggaacaaaagtaacatctttagagtcgggcatttaagcaacatatcttgctac 1353
                                                                                                                                                                                                                                                             1234 tccatttcattggataacttaaaaccctccagagtgtactgtttacaagtccaggcacaa 1293
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                                                                                                                                                                                                                         661 TCCATTTCATTGGATAACTTAAAACCCTCCAGAGTGTACTGTTTACAAGTYCAGGCACAA
                                                                                                                                                                                                                                                                                                                                                                      601 TATGTCCATTACTGGGAAAAAGGAGGAATCCAACAGGTCAAAGGCCCTTTCAGAAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           994 cgagctgagctgggagcactccattctgcctgggtgacaatgccttggtttcaacactat 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAGCTGAGCTGGGAGCACTCCATTCTGCCTGGGTGACAATGCCTTTGGTTTCAACACTAT 480
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                                                                            CTGCTTTGGAACAAAGTAACATCTTTAGAGTCGGGCATTTAAGCAACATATCTTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGGCCGAMATCATGTCCATAGGGGTGAATTGTACACAGATCACAGCAACARAGTGTGAC
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Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
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                                                                                                                                                                                                                                                                                                          1221 tttcagaagcaactccatttcattggataacttaaaaccctccagagtgtactgtttaca 1280
                                                                                                                                                                                  1281 agtccaggcacaactgctttggaacaaaagtaacatctttagagtcgggcatttaagcaa 1340
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                                                                                                                    871 AGTCCAGGCACCACTGCTTTGGAACAAAAGTAAMATCTTTAGAGTCGGGMATTTAAGCAA 812
                                                                                                                                                                                                                                                               931 TTTCAGAAGCAACTCCATTTCATTGGATCACTTAATTTCCTCCAGAGTGTACTGTTTACA 872
                                                                                                                                                                                                                                                                                                                                                                                                       989 CCTTTTTTGTTATTATGTCCATRACTGG--AAAAAGGAGAATCCAACAGGTCAAAGGCCC 932
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                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 955)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
   Genoscope - Centre National de Sequencage
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1156 acggcctttttttgttattatgtccattactgggaaaaaggaggaatccaacaggtcaaa 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736 ctgcccgctcctcagcacccgaagattcgcctgtacaacgcagagcaggtcctgagttgg 795
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                                                                                                                                                               540 CCTTGGTTTCAACACTATCGGAATGTGACTGTCGGGCCTCCAGAAAACATTGAGGTGACC 599
                                                                                                                                                                                                                                                                           480 AATGTCACTCTACGCCTTCGAGCTGAGCTGGGAGCACTCCATTCTGCCTGGGTGACAATG 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              796 gagccagtggccctgagcaatagcacgaggcctgttgtctaccgagtgcagtttaaatac 855
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/note="Vector: pcMVSPORT 6; Site_1: Not!; lst strand cDNA
/note="Vector: pcMVSPORT 6; Site_1: Not!; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
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                                     1285 caggcacaactgctttggaacaaaagtaacatctttagagtcgggcatttaagcaacata 1344
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                                                                                                                    950 AGARGCAACTCCATTTCATTGGATAACTTAAAACCCTCCAGAGTGTACTGTTTACAAGTC 891
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                                                                                                                                                                                                                                                                    Local
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/note="Vector: pcMvSPoRT 6; Site_I: NotI; 1st strand.cDNA
/note="Vector: pcMvSPoRT 6; Site_I: NotI; 1st strand.cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPoRT 6
/vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Dive
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 969)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                      Homo sapiens
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                                                                                                                                       541 CCAGGAGAAGGCTCCCTCATCATCAGGTTCTCCTCTCTCCTTTGACATCGCTGATACCTCC
                                                                                                                                                                                                                                                                 481 CCTTGGTTTCAACACTATCGGAATGTGACTGTCGGGCCTCCAGAAAACATTGAGGTGACC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CTGCTGCTGCTCGGAGTCTTCGCCGCCGCCGCCGCCGCCGCCAGACCCTCTTTCCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Limid 1: fliang@lifetech.com URL:
http://falllength.invitrogen.com"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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260 c 208 g 217 t 1
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                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and
                                                                                                                                                                                                                                                                            Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                cloned into the Not I and Eco RV sites of the pCMVSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CS0DI009YE16"
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/db_xref="taxon:9606"
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                                                                                                    40.6%; Score 897.8; DB 9; 98.2%; Pred. No. 2.3e-150;
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     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1399 atctccgtgggaacattttcgttgctgtcggtgctggcaggagcctgtttcttcctggtc 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1339 aacatatcttgctacgaaacaatggcagatgcctccactgagcttcagcaagtcatcctg 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1279 caagtccaggcacaactgctttggaacaaaagtaacatctttagagtcgggcatttaagc 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1159 gcctttttttgttattatgtccattactgggaaaaaggaggaatccaacaggtcaaaggc 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1099 ggagaaggctccctcatcatcaggttctcctctcccctttgaccatcgctgatacctccacg 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039 tggtttcaacactatcggaatgtgactgtcgggcctccagaaaacattgaggtgacccca 1098
                                                                                                                                                                                                                                                                                                                                         1519 atagaagagtatttaaaagac 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1219 cctttcagaagcaactccatttcattggataacttaaaaccctccagagtgtactgttta 1278
                                                                                                                                                                                                                                                                                               900 ATAGAAGAGTATTTAAAARAC 920
                                                                                                                                                                                                                                                                                                                                                                                        840 CTGAAATAWAAAGGCCTGATTAAATACTGGTTTCACACTCCACCAAGCATCCCATTACAG 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       780 ATCTCCGTGGGAAAAWTTTCGTTGCTGTCGGTGCTGGCAGGAGCCTGTTTCTTCCTGGTC 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720 AACATATCTTGCTACGAAACAATGGCAGATGCCTCCACTGAGCTTCAGCAAGTCATCCTG 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600 CCTTTCAGAAGCAACTCCATTTCATTGGATAACTTAAAACCCTCCAGAGTGTACTGTTTA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540 GCCTTTTTTTGTTATTATGTCCATTACTGGGAAAAAAGAGGAATCCAACARGTCAAAGGC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 GGAGAAGGCTCCCTCATCATCAGGTTCTCCTCTCCCTTTGACATCGCTGATACCTCCACG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      660 CAAGTCCAGGCACAAMTGCTTTGGAACAAAARTAAMATCTTTAGAGTCGGGCATTTAAGC 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 TGGTTTCAACACTATCGGAATGTGACTGTCGGGCCTCCAGAAAACATTGAGGTGACCCCA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 GTCACTCTACGCCTTCGAGCTGAGCTGGGAGCACTCCATTCTGCCTGGGTGACAATGCCT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    979 gtcactctacgccttcgagctgagctgggagcactccattctgcctgggtgacaatgcct 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 GACAGTAAATGGTTCACGGCCGACATCATGTCCATAGGGGTGAATTGTACACARATCACA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 gacagtaaatggttcacggccgacatcatgtccataggggtgaattgtacacagatcaca 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 CCAGTGGCCCTGAGCAATAGCACGAGGCCTGTTGTCTACCAAGTGCAGTTTAAATACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   799 ccagtggccctgagcaatagcacgaggcctgttgtctaccgagtgcagtttaaatacacc 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 CCCGCTCCTCAGCACCCGAAGATTCGCCTGTACAACGCAGAGCAGGTCCTGAGTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    739 cccgctcctcagcacccgaagattcgcctgtacaacgcagagcaggtcctgagttgggag 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              679 ctgctgctcggagtcttcgccgccgccgccgcgcgccccgccagaccctctttcccagctg 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTGCTGCTCGGAGTCTTCGCCGCCGCCGCCGCCGCCGCCARAMCCWCTTTCCCAGCTG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACCTGAGCCGCCGCGGGCCCCGGGGCCCATGCGACCGCTGCTGTTGGTCGCTGCTG 60
Homo sapiens
                                                    EST
                            numan
                                                                       AL551114.1 GI:12888746
                                                                                                                         prime, mRNA sequence
                                                                                                                                           AL551114 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI066YD14
                                                                                                                                                                             AL551114
                                                                                                                                                                        mRNA
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1000 gagctgggagcactccattctgcctgggtgacaatgccttggtttcaacactatcggaat 1059
                                                                                                                                                1060 gtgactgtcgggcctccagaaaacattgaggtgaccccaggagaaggctccctcatcatc 1119
                                                                                          481 GTGACTGTCGGGCCTCCAGAAAACATTGAGGTGACCCCAGGAGAAGGCTCCCTCATCATC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640 cccggggccatgcgacgctgctgctgtggtggctgctgctgctcggagtcttcgcc 699
                                                                                                                                                                                                             421 GAGCTGGGAGCACTCCATTCTGCCTGGGTGACAATGCCCTTGGTTTCAACACTATCGGAAT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ATTCGCCTGTACAACGCAGAGCAGGTCCTGAGTTGGGAGCCAGTGGCCCTGAGCAATAGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                760 attcgcctgtacaacgcagagcaggtcctgagttgggagccagtgggccctgagcaatagc 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        700 gccgccgccgccgcccgccagaccctctttcccagctgcccgctcctcagcacccgaag 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581 tgagcggctccgcgg-accccgagcggggccccggcgacctgagccgccgccgaccg 639
                                                                                                                                                                                                                                                                                                                                     361 GCCGCCAGTCCCTCAGCAGGCTTCCCAATGGATTTCAATGTCACTCTACGCCTTCGAGCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CCCGGGGCCATGCGACGCTGCTGCTGGTCGCTGCTGCTGCTCGGAGTCTTCGCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gccgccagtccctcagcaggcttcccaatggatttcaatgtcactctacgccttcgagct 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACATCATGTCCATAGGGGTGAATTGTACACAGATCACAGCAACAGAGTGTGACTTCACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gacatcatgtccataggggtgaattgtacacagatcaccagcaacagagtgtgacttcact 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGAGGCCTGTTGTCTACCAAGTGCAGTTTAAATACACCGACAGTAAATGGTTCACGGCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acgaggcctgttgtctaccgagtgcagtttaaatacaccgacagtaaatggttcacggcc 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li,W.B., Gruber,C., Jessee,J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 40.5%;
Similarity 99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloned into the Not I and Eco RV Sites of the PCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockyllle, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://fulllength.invitrogen.com"
a 274 c 226 g 213 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CS0DI066YD14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="LTI_NFL006_PL2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fliang@lifetech.com URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jessee, J. and Polayes, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 896.6; DB 9; Pred. No. 3.7e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7e-150;
ches 2;
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         Matches 927;
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1480 aaatactggtttcacactccaccaa 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1360 atggcagatgcctccactgagcttcagcaagtcatcctgatctccgtgggaacattttcg 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1240 tcattggataacttaaaaccctccagagtgtactgtttacaagtccaggcacaactgctt 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    900 WAATACTGGTTTCACACTCCACCAA 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        841 TTGCTGTCGGTGCTGGCAGGAGCCTGTTTCTTCCTGGTCCTGAAATATAGAGG-CTGAAT 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 TGGAACAAAGTAACATCTTTAGAGTCGGGCATTTAAGCAACATATCTTGCTACGAAACA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 TCATTGGATAACTTAAAACCCTCCAGAGTGTACTGTTTACAAGTCCAGGCACAACTGCTT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CATTACTGGGAAAAAGGAGGAATCCAACAGGTCAAAGGCCCTTTCAGAAGCAACTCCATT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 40.4%;
Local Similarity 99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tggaacaaaagtaacatctttagagtcgggcatttaagcaacatatcttgctacgaaaca 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCAGATGCCTCCACTGAGCTTCAGCAAGTCATCCTGATCTCCGTGGGAACATTTTCG 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL562646 DTI_NFL003_NBC3 Homo sapiens cDNA clone CSODC016YC03 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 931)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL562646.1 GI:12911272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
         Conservative
                                                                                                                                                                                 by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="neuroblastoma cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="LTI_NFL003_NBC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="CS0DC016YC03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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         4; Mismatches
                                      Score 895; DB 9;
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            2158 taatttaagattttgttttttaaactggaaataaaa 2192
                                                                                                                                                                                                                                                                                1918 ctaaaaaggcatgtaattgcttgttagcaaaatggatatgacacatctctgatacttttt 1977
                                                                                                                                                                                                                                                                                                                                                 1858 atcaaattccagaatgattttacggagatatcccaggaaaattaaggcttctctcttaaaca 1917
                                                                                                                                                                                                                                                                                                                                                                                               1738 tttccagagaccagtattcccttttgctgcctctaaaaggcctgtccctgcagacatgag 1797
                                                                            2098 toatgtacatccatggtgtgctggcttaaaatgtaattaatcttgtaaatatactcctag 2157
                                                                                                                                                 2038 agccggagccccttgggcaggtcacaccacctgtcccagcgagggacactgagtggccct 2097
                                                                                                                                                                                                             1978 tcattattggtttgggctgagcagtcagaagacctggtcgtcgtcttgactttggccaaatg 2037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1318 tttagagtcgggcatttaagcaacatatcttgctacgaaacaatggcagatgcctccact 1377
                                                                                                                                                                                            214 TCATTATTGGTTGGGCTGAGCAGTCAGAAGACCTGGTCGTCGTCTTGACTTTGGCAAATG 155
                                                                                                                                                                                                                                                              274 CTAAAAAGGCATGTAATTGCTTGTTAGCAAAATGGATATGACACATCTCTGATACTTTTT 215
                                                                                                                                                                                                                                                                                                                                 334 ATCAAATTCCAGAATGATTTTACGGAGATATCCCCAGGAAAATTAAGGCTTCTCTTAAACA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 TITCCAGAGACCAGTATTCCCTTTTGCTGCCTCTAAAAGGCCTGTCCCTGCAGACATGAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572 TCGTTTCCGGAAAAGGAGCAAGAAGATGTTCTCCAAACGCTTTGAACCAAAGCATGGGCC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632 GAGGCCTTGGACAAGGACAGCTCACCAAAGGATGACGTCTGGGACTCTGTGTCCATTATC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     751 GGAGCCTGTTTCCTTGGTCCTGAAATATAGAGGCCTGATTAAATACT-GKTTCACACT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          871 TTTAGAGTCGGGCATTTAAGCAACATATCTTGCTACGAAACAATGGCAGATGCCTCCACT 812
                                                                   94
 34
TAATTTAAGATTKT-TTTTTAAACTGGAAATAAAA 1
                                                             AGCCGGAGCCCCTTGGGCAGGTCACACAACCTGTCCCAGCGAGGGACACTGAGTGGCCCH 95
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Search completed: September 10, 2002, 17:35:07 Job time: 3112 sec

